

What is claimed is:

1. - 48. (cancelled)

49. (New) A method for detecting coronary artery disease in a human test subject, comprising:

a) Quantifying in RNA of a blood sample from said test subject, a level of RNA encoded by the gene CRTAM (cytotoxic and regulatory T cell molecule) in said sample; and

b) Comparing said quantified level with a quantified level of control RNA encoded by said gene in RNA of blood samples from control subjects;

wherein said comparison of said quantified level of step (a) with said quantified level of said control subjects is indicative of coronary artery disease in said human test subject.

50. (New) The method of claim 49, wherein said blood sample of step (a) and said blood samples from said control subjects in step (b) have not been fractionated into cell types.

51. (New) The method of claim 49, wherein said blood sample of step (a) and said blood samples from said control subjects in step (b) are unfractionated samples of lysed blood.

52. (New) The method of any of claims 49, 50 or 51, wherein said quantifying of said level of said RNA encoded by said gene in step (a) is effected by quantifying said RNA relative to a housekeeping gene.

53. (New) The method of any of claims 49, 50 or 51, wherein said quantifying of said level of said RNA encoded by said gene in step (a) is effected by quantification of cDNA corresponding to said RNA.

54. (New) The method of any of claims 49, 50 or 51, wherein said control subjects do not have coronary artery disease and said comparison of step (b) results in a statistically significant difference.

55. (New) The method of any of claims 49, 50 or 51, wherein said control subjects have been diagnosed as having coronary artery disease and said comparison results in a statistically significant similarity.

56. (New) The method of any of claims 49, 50 or 51, wherein said quantifying of said level of said RNA encoded by said gene in step (a) is determined using quantitative real-time RT-PCR.
57. (New) The method of any of claims 49, 50 or 51, wherein said quantifying of said level of said RNA encoded by said gene in step (a) is determined using an array.